50. The method according to claim **47**, wherein the antigen-binding molecule comprises:

(a) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:289; and a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:310; or

(b) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:289; and a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:297; or

(c) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:289; and a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:294; or

(d) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:289; and a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:299; or

(e) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:289; and a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:301; or

(f) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:289; and a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:302; or

(g) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:285; and a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:287; or

(h) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:52; and a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:57; or

(i) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:62; and a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:66; or

(j) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:32; and a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:40.

51. The method according to claim **47**, wherein the cancer is selected from: a cancer comprising cells expressing VISTA, a cancer comprising infiltration of cells expressing VISTA, a cancer comprising cancer cells expressing VISTA, a hematological cancer, leukemia, acute myeloid leukemia, lymphoma, B cell lymphoma, T cell lymphoma, multiple myeloma, mesothelioma, a solid tumor, lung cancer, non-small cell lung carcinoma, gastric cancer, gastric carcinoma, colorectal cancer, colorectal carcinoma, colorectal adenocarcinoma, uterine cancer, uterine corpus endometrial carcinoma, breast cancer, triple negative breast invasive carcinoma, liver cancer, hepatocellular carcinoma, pancreatic cancer, pancreatic ductal adenocarcinoma, thyroid cancer, thymoma, skin cancer, melanoma, cutaneous melanoma, kidney cancer, renal cell carcinoma, renal papillary cell carcinoma, head and neck cancer, squamous cell carcinoma of the head and neck (SCCHN), ovarian cancer, ovarian carcinoma, ovarian serous cystadenocarcinoma, prostate cancer and/or prostate adenocarcinoma.

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